



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 181503

TO: James Schultz
Location: rem/2D18/2C18
Art U. : 1035
Wednesday, March 15, 2006

Case Serial Number: 10/726422

From: Paul Schulwitz
Location: Biotech-Chem Library
REM-1A65
Phone: 571-272-2527

Paul.schulwitz@uspto.gov

See

Examiner Schultz,

Please review the attached search results.

If you have any questions or if you would like to refine the search query, please feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
REM-1A65
571-272-2527

BEST AVAILABLE COPY

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181503

MS

STIC-Biotech/ChemLib

From: Schultz, James
Sent: Monday, March 06, 2006 5:25 PM
To: STIC-Biotech/ChemLib
Subject: Seq Search 10/726,422

Hello,
Could you please run a standard, length limited nucleotide sequence search against SEQ ID NO: 1 in the above entitled application, which returns hits between 10 and 40 nucleotides?

Thanks,
Doug Schultz

James Douglas Schultz, PhD
Primary Examiner
AU 1635 (Biotechnology)
United States Patent and Trademark Office
(Office) REM 2D18
(Mail) REM 2C18
(571) 272-0763

RECEIVED
MAR - 7 2006
STIC

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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REFERENCE
AUTHORS
Unclassified.
1 (bases 1 to 24)
Zetter, B.R. and Bao, L.

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TITLE      Method for prognosis of prostate cancer
JOURNAL    Patent: US 5858681-A 4 12-JAN-1999;
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Qy 356 ACCCTGACTGAAGGTCAGCATTT 379
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Db 24 ACCCTGACTGAAGGTCAGCATTT 1

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DEFINITION Sequence 8 from patent US 5831033.
ACCESSION  AR052451
VERSION     AR052451.1 GI:5975815
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 24)
AUTHORS    Zetter,B.R. and Bao,L.
TITLE      Human thymosin .beta.15 gene, protein and uses thereof
JOURNAL    Patent: US 5831033-A 8 03-NOV-1998;
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TATCAGCTAGTGGCTGCACCGCG 24

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ACCESSION  AR052452
VERSION     AR052452.1 GI:5975816
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 24)
AUTHORS    Zetter,B.R. and Bao,L.
TITLE      Human thymosin .beta.15 gene, protein and uses thereof
JOURNAL    Patent: US 5831033-A 9 03-NOV-1998;
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ACCESSION  I63533
VERSION     I63533.1 GI:2481106
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 24)
AUTHORS    Zetter,B.R. and Bao,L.
TITLE      Human thymosin .beta.15 gene, protein and uses thereof
JOURNAL    Patent: US 5663071-A 8 02-SEP-1997;
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DEFINITION Sequence 9 from patent US 5663071.
ACCESSION  I63534
VERSION     I63534.1 GI:2481107
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 24)
AUTHORS    Zetter,B.R. and Bao,L.
TITLE      Human thymosin .beta.15 gene, protein and uses thereof
JOURNAL    Patent: US 5663071-A 9 02-SEP-1997;
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Qy 356 ACCCTGACTGAAGGTCAGCATTT 379
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Db 24 ACCCTGACTGAAGGTCAGCATTT 1

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DEFINITION Sequence 8 from patent US 5721337.
ACCESSION  I89355
VERSION     I89355.1 GI:3409295
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 24)
AUTHORS    Zetter,B.R. and Bao,L.
TITLE      Human thymosin .beta.15

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Db 1 TATCAGCTAGTGGCTGCACCCGCG 24
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LOCUS I89356 24 bp DNA linear PAT 10-AUG-1998
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ACCESSION I89356
VERSION I89356.1 GI:3409296
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Zetter,B.R. and Bao,L.
TITLE Human thymosin .beta.15
JOURNAL Patent: US 5721337-A 9 24-FEB-1998;
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QY 356 ACCCTGACTGAAAGTCAGCATTT 379
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RESULT 9
LOCUS AR370452 24 bp mRNA linear PAT 12-SEP-2003
DEFINITION Sequence 8 from patent US 6300479.
ACCESSION AR370452
VERSION AR370452.1 GI:34607137
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Zetter,B.R. and Bao,L.
TITLE Antibodies specific for human thymosin .beta.15 protein and uses thereof
JOURNAL Patent: US 6300479-A 8 09-OCT-2001;
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DEFINITION Sequence 9 from patent US 6300479.
ACCESSION AR370453
VERSION AR370453.1 GI:34607138
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Zetter,B.R. and Bao,L.
TITLE Antibodies specific for human thymosin .beta.15 protein and uses thereof
JOURNAL Patent: US 6300479-A 9 09-OCT-2001;
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Best Local Similarity 100.0%; Pred. No. 4.6e+05;
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Db 24 ACCCTGACTGAAAGTCAGCATTT 1
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ACCESSION AX645186
VERSION AX645186.1 GI:28611008
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Zetter,B.R. and Bao,L.
TITLE Thymosin B15 as a marker in diagnosis and prognosis of cancer
JOURNAL Patent: EP 1270745-A 3 02-JAN-2003;
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Db 1 TATCAGCTAGTGGCTGCACCCGCG 24
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DEFINITION Sequence 4 from Patent EP1270745.
ACCESSION AX645187
VERSION AX645187.1 GI:28611009
KEYWORDS
SOURCE unidentified
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ORGANISM unidentified
REFERENCE 1
AUTHORS Zetter,B.R. and Bao,L.
TITLE Thymosin B15 as a marker in diagnosis and prognosis of cancer
JOURNAL Patent: EP 1270745-A 4 02-JAN-2003;
CHILDREN'S MEDICAL CENTER CORPORATION (US)
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QY 356 ACCCTGACTGAAAGTTCAGCATTT 379
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DEFINITION Sequence 374 from patent US 5677149.
ACCESSION I69104
VERSION I69104.1 GI:2831226
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 36)
AUTHORS Bauer,S.Christopher., Abrams,M.Allen., Braford-Goldberg,S.Ruth.,
Caparon,M.Helena., Easton,A.Michael., Klein,B.Kure.,
McKearn,J.Patrick., Olins,P., Paik,K., Polazzi,J. and
Thomas,J.Warren.
TITLE Interleukin-3 (IL-3) mutant polypeptides and their recombinant
production
JOURNAL Patent: US 5677149-A 374 14-OCT-1997;
FEATURES
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DEFINITION Sequence 374 from patent US 6479261.
ACCESSION AR253702
VERSION AR253702.1 GI:27302130
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 36)
AUTHORS Bauer,S.C., Abrams,M.A., Braford-Goldberg,S.R., Caparon,M.H.,
Easton,A.M., Klein,B.K., McKearn,J.P., Olins,P., Paik,K.,
Polazzi,J. and Thomas,J.W.
TITLE Methods of using interleukin-3 (IL-3) mutant polypeptides for
ex-vivo expansion of hematopoietic stem cells
JOURNAL Patent: US 6479261-A 374 12-NOV-2002;

Pharmacia Corporation; St. Louis, MO
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RESULT 15
LOCUS AX696757 36 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 374 from Patent EP1283264.
ACCESSION AX696757
VERSION AX696757.1 GI:29419867
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Bauer,S.C., Abrams,M.A., Braford-Goldberg,S.R., Caparon,M.H.,
Easton,A.M., Klein,B.K., McKearn,J.P., Olins,P.O., Paik,K.,
Polazzi,J.O. and Thomas,J.W.
TITLE Interleukin-3 (il-3) mutant polypeptides
JOURNAL Patent: EP 1283264-A 374 12-FEB-2003;
G.D. SEARLE & CO. (US)
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Search completed: March 12, 2006, 06:43:56
Job time : 2714 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 12, 2006, 04:32:20 ; Search time 484 Seconds
(without alignments)
5673.251 Million cell updates/sec

Title: US-10-726-422-1

Perfect score: 412

Sequence: 1 TATCAGCTAGTGGTGCAC.....AAATGTGTTTCCACTGCTC 412

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 4583304

Minimum DB seq length: 10

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	24	5.8	24	2	AAT98003 Human thy
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C 19	20.4	5.0	36	12	ADI58589 Human int

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21	19.6	4.8	35	3	AC63564	MiniSeqe
22	19.6	4.8	40	6	ABL35524	Immunostl
23	19.4	4.7	33	10	ADC36204	Weed cont
24	19.4	4.7	39	14	ADZ71344	Novel cyb
25	19.4	4.7	40	6	ABK92523	E. coli D
26	19.2	4.7	33	2	AAX81507	Primer us
27	19	4.6	36	10	ADC02924	Ex vivo s
28	19	4.6	36	12	ADI58599	Human int
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30	18.8	4.6	36	10	ADC02918	Ex vivo s
31	18.8	4.6	36	10	ADC02916	Ex vivo s
32	18.8	4.6	36	10	ADC02920	Ex vivo s
33	18.8	4.6	36	12	ADI58601	Human int
34	18.8	4.6	36	12	ADI58591	Human int
35	18.8	4.6	36	12	ADI58593	Human int
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41	18.4	4.5	40	6	ABL91386	Chlamydia
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ALIGNMENTS

RESULT 1

AAT98004/c

ID AAT98004 standard; cDNA; 24 BP.

AC AAT98004;

XX AAT98004;

DT 10-MAR-1998 (first entry)

DE Human thymosin beta-15 reverse primer T-beta 15.

XX Human thymosin beta 15; G-actin; cell motility; adenocarcinoma; ss;

KW Human; thymosin beta 15; G-actin; cell motility; adenocarcinoma; ss;

KW metastasis; PCR; amplification; primer; detection; diagnosis; cancer.

XX Synthetic.

OS Homo sapiens.

XX Homo sapiens.

PN US5663071-A.

XX US5663071-A.

PD 02-SEP-1997.

PF 17-JUN-1996; 96US-00664856.

PR 17-JUN-1996; 96US-00664856.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Zetter BR, Bao L;

XX WPI; 1997-447933/41.

XX DNA encoding thymosin beta-15 - which binds G-actin and regulates cell

PT motility, useful for detecting cancers in e.g. prostate, lung tissues,

XX especially metastatic cancers.

XX Example; Col 12; 22pp; English.

PS Primers AAT98003-T98008 are used to PCR amplify the nucleotide sequence

CC encoding a human thymosin beta-15, a novel protein that binds and

CC sequesters G-actin and also regulates cell motility in prostatic

CC carcinoma cells. The sequence was isolated from a cDNA library

CC constructed from polyA RNA purified from a highly metastatic cell line

CC AT3.1 derived from Dunning R3327 rat prostatic adenocarcinoma cells. The

CC nucleic acid and proteins can be used to detect increased expression of
 CC the thymosin beta 15 gene in non-testicular cells which has a high
 CC correlation to cancers, e.g. prostate, lung, melanoma and breast cancers,
 CC especially metastatic cancers
 XX

SQ Sequence 24 BP; 6 A; 5 C; 6 G; 7 T; 0 U; 0 Other;
 Query Match 5.8%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 356 ACCCTGACTGAAGGTCAGCATTT 379
 |||||
 Db 24 ACCCTGACTGAAGGTCAGCATTT 1

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 ID AAT98003 standard; cDNA; 24 BP.
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 AC AAT98003;
 XX
 DT 10-MAR-1998 (first entry)
 XX
 DE Human thymosin beta-15 forward primer T-beta 15.
 XX
 KW Human; thymosin beta 15; G-actin; cell motility; adenocarcinoma; ss;
 KW metastasis; PCR; amplification; primer; detection; diagnosis; cancer.
 XX

OS Synthetic.
 OS Homo sapiens.

PN US5663071-A.
 XX
 PD 02-SEP-1997.

PF 17-JUN-1996; 96US-00664856.
 XX
 PR 17-JUN-1996; 96US-00664856.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.

PI Zetter BR, Bao L;
 XX
 DR WPI, 1997-447933/41.

XX DNA encoding thymosin beta-15 - which binds G-actin and regulates cell
 PT motility, useful for detecting cancers in e.g. prostate, lung tissues,
 PT especially metastatic cancers.

PS Example; Col 12; 22pp; English.
 XX
 CC Primers AAT98003-T98008 are used to PCR amplify the nucleotide sequence
 CC encoding a human thymosin beta-15, a novel protein that binds and
 CC sequesters G-actin and also regulates cell motility in prostatic
 CC carcinoma cells. The sequence was isolated from a cDNA library
 CC constructed from polyA RNA purified from a highly metastatic cell line
 CC AT3.1 derived from Dunning R3327 rat prostatic adenocarcinoma cells. The
 CC nucleic acid and proteins can be used to detect increased expression of
 CC the thymosin beta 15 gene in non-testicular cells which has a high
 CC correlation to cancers, e.g. prostate, lung, melanoma and breast cancers,
 CC especially metastatic cancers

XX Sequence 24 BP; 4 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 5.8%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATCAGCTAGTGGCTGCACCCGCG 24
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 Db 1 TATCAGCTAGTGGCTGCACCCGCG 24

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 ID AAV05152 standard; cDNA; 24 BP.
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 AC AAV05152;

DT 24-JUN-1998 (first entry)
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 DE Human thymosin beta-15 PCR primer.

XX Human thymosin beta 15; G-actin; cell motility; prostatic carcinoma;
 KW antibody; cancer; diagnosis; prognosis; prostate; lung; melanoma; breast;
 KW ss; PCR; primer; amplification.

XX Synthetic.
 OS Homo sapiens.
 PN WO9748982-A1.

XX 24-DEC-1997.

PF 13-JUN-1997; 97WO-US010306.

PR 17-JUN-1996; 96US-00664857.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Zetter BR, Bao L;

XX WPI; 1998-120303/11.

XX Diagnosis and prognosis of cancer - by measuring levels of thymosin beta
 PT 15 in a biological sample.

XX Disclosure; Page 18; 41pp; English.

XX Thymosin beta 15 primers AAV05151 and AAV05152 are used for the
 CC amplification of thymosin beta 15 gene. Human thymosin beta 15 has the
 CC ability to bind and sequester G-actin like other members of the thymosin
 CC beta family, it also directly regulates cell motility in prostatic
 CC carcinoma cells. Thymosin beta 15 can be detected in bodily fluids using
 CC antibodies, PCR primers and probes. A correlation between expression of
 CC human thymosin beta 15 and disease state in a number of cancers has been
 CC demonstrated. This can be used for the diagnosis and prognosis of
 CC prostate, lung, melanoma or breast cancer

XX Sequence 24 BP; 6 A; 5 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 5.8%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 356 ACCCTGACTGAAGGTCAGCATTT 379
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 Db 24 ACCCTGACTGAAGGTCAGCATTT 1

RESULT 4
 AAV05151
 ID AAV05151 standard; cDNA; 24 BP.
 XX
 AC AAV05151;

XX 24-JUN-1998 (first entry)

XX Human thymosin beta-15 PCR primer.

XX Human thymosin beta 15; G-actin; cell motility; prostatic carcinoma;
 KW antibody; cancer; diagnosis; prognosis; prostate; lung; melanoma; breast;
 KW ss; PCR; primer; amplification.

XX Synthetic.

Query Match 5.8%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATCAGCTAGTGGCTGCACCCGCG 24
|||||
Db 1 TATCAGCTAGTGGCTGCACCCGCG 24

RESULT 7
AAV15084
ID AAV15084 standard; DNA; 24 BP.
XX
AC AAV15084;
XX
DT 20-MAY-1998 (first entry)
XX
DE Human thymosin beta 15 PCR forward primer SEQ ID NO:8.
XX
KW Human; thymosin beta 15; G-actin; cell motility; regulation;
KW prostatic carcinoma; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
FN US5721337-A.
XX
PD 24-FEB-1998.
XX
PF 14-FEB-1997; 97US-00801796.
XX
PR 17-JUN-1996; 96US-00664856.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Bao L, Zetter BR;
XX
DR WPI; 1998-168472/15.
XX
PT Human thymosin beta-15 - regulating prostatic carcinoma cell motility.
XX
PS Disclosure; Col 12; 22pp; English.
XX
FN US5721337-A.
XX
PD 24-FEB-1998.
XX
PF 14-FEB-1997; 97US-00801796.
XX
PR 17-JUN-1996; 96US-00664856.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Bao L, Zetter BR;
XX
DR WPI; 1998-168472/15.
XX
PT Human thymosin beta-15 - regulating prostatic carcinoma cell motility.
XX
PS Disclosure; Col 12; 22pp; English.

CC The present sequence represents a PCR primer for human thymosin beta 15,
CC used in the present invention describing human thymosin beta 15. The
CC present invention also describes: antibodies and antibody fragments
CC specific for thymosin beta 15; vectors containing the nucleic acids; and
CC a method for treating a neoplastic cell expressing human thymosin beta 15
CC by administering a compound that inhibits the activity or production of
CC thymosin beta 15, preferably an antisense oligonucleotide, ribozyme, G-
CC antibody or antibody fragment. Thymosin beta 15 binds and sequesters G-
CC actin and directly regulates cell motility in prostatic carcinoma cells
XX
SQ Sequence 24 BP; 6 A; 5 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 5.8%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATCAGCTAGTGGCTGCACCCGCG 24
|||||
Db 1 TATCAGCTAGTGGCTGCACCCGCG 24

RESULT 8
AAV15085/c
ID AAV15085 standard; DNA; 24 BP.
XX
AC AAV15085;
XX
DT 20-MAY-1998 (first entry)
XX
DE Human thymosin beta 15 PCR forward primer SEQ ID NO:8.
XX
KW Human; thymosin beta 15; G-actin; cell motility; regulation;
KW prostatic carcinoma; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
FN US5721337-A.
XX
PD 24-FEB-1998.
XX
PF 14-FEB-1997; 97US-00801796.
XX
PR 17-JUN-1996; 96US-00664856.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Bao L, Zetter BR;
XX
DR WPI; 1998-168472/15.
XX
PT Human thymosin beta-15 - regulating prostatic carcinoma cell motility.
XX
PS Disclosure; Col 12; 22pp; English.

CC The present sequence represents a PCR primer for human thymosin beta 15,
CC used in the present invention describing human thymosin beta 15. The
CC present invention also describes: antibodies and antibody fragments
CC specific for thymosin beta 15; vectors containing the nucleic acids; and
CC a method for treating a neoplastic cell expressing human thymosin beta 15
CC by administering a compound that inhibits the activity or production of
CC thymosin beta 15, preferably an antisense oligonucleotide, ribozyme, G-
CC antibody or antibody fragment. Thymosin beta 15 binds and sequesters G-
CC actin and directly regulates cell motility in prostatic carcinoma cells
XX
SQ Sequence 24 BP; 4 A; 8 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 5.8%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 356 ACCCTGACTGAAGGTCAGCATTT 379
|||||
Db 24 ACCCTGACTGAAGGTCAGCATTT 1

RESULT 9
AAZ86879
ID AAZ86879 standard; cDNA; 24 BP.
XX
AC AAZ86879;
XX
DT 03-MAY-2000 (first entry)
XX
DE PCR primer for human thymosin beta15 coding sequence.
XX
KW Thymosin beta15; human; expression inhibitor; antibody; diagnosis;
KW cancer; prostate cancer; therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
FN US6017717-A.
XX
PD 25-JAN-2000.
XX
PF 29-APR-1998; 98US-00069484.
XX
PR 14-FEB-1997; 97US-00801796.
XX
PR 17-SEP-1997; 97US-00931877.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX

Query Match 5.8%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 356 ACCCTGACTGAAGGTCAGCATTT 379
|||||
Db 24 ACCCTGACTGAAGGTCAGCATTT 1

RESULT 9
AAZ86879
ID AAZ86879 standard; cDNA; 24 BP.
XX
AC AAZ86879;
XX
DT 03-MAY-2000 (first entry)
XX
DE PCR primer for human thymosin beta15 coding sequence.
XX
KW Thymosin beta15; human; expression inhibitor; antibody; diagnosis;
KW cancer; prostate cancer; therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
FN US6017717-A.
XX
PD 25-JAN-2000.
XX
PF 29-APR-1998; 98US-00069484.
XX
PR 14-FEB-1997; 97US-00801796.
XX
PR 17-SEP-1997; 97US-00931877.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX

Query Match 5.8%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 356 ACCCTGACTGAAGGTCAGCATTT 379
|||||
Db 24 ACCCTGACTGAAGGTCAGCATTT 1

PI Bao L, Zetter BR;
 XX WPI; 2000-136675/12.
 XX Inhibiting thymosin beta 15 expression, useful for diagnosing and
 XX treating cancer.
 PT
 XX Example; Col 12; 22pp; English.

PS This sequence represents a PCR primer for DNA encoding the human thymosin

CC betal5 protein. The invention relates to a method for inhibiting thymosin
 CC betal5 expression in a cell comprising administering an antibody or
 CC antibody fragment. The method is useful for treating and diagnosing
 CC cancer, particularly prostate cancer

XX Sequence 24 BP; 4 A; 8 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 5.8%; Score 24; DB 3; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATCAGTAGTGGCTGCACCCGCG 24
 |||||
 DB 1 TATCAGTAGTGGCTGCACCCGCG 24

RESULT 10
 AAZ86880/c
 ID AAZ86880 standard; cDNA; 24 BP.

XX AAZ86880;

AC 03-MAY-2000 (first entry)

DT PCR primer for human thymosin betal5 coding sequence.

DE Thymosin betal5; human; expression inhibitor; antibody; diagnosis;
 KW cancer; prostate cancer; therapy; PCR primer; ss.

XX Homo sapiens.

OS US6017717-A.

XX 25-JAN-2000.

XX 29-APR-1998; 98US-00069484.

XX 14-FEB-1997; 97US-00801796.

PR 17-SEP-1997; 97US-00931877.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Bao L, Zetter BR;

XX WPI; 2000-136675/12.

XX Inhibiting thymosin beta 15 expression, useful for diagnosing and
 XX treating cancer.

XX Example; Col 12; 22pp; English.

PS This sequence represents a PCR primer for DNA encoding the human thymosin
 CC betal5 protein. The invention relates to a method for inhibiting thymosin
 CC betal5 expression in a cell comprising administering an antibody or
 CC antibody fragment. The method is useful for treating and diagnosing
 CC cancer, particularly prostate cancer

XX Sequence 24 BP; 6 A; 5 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 5.8%; Score 24; DB 3; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 ACCCTGACTGAAGGTCAGCATTT 379
 |||||
 DB 24 ACCCTGACTGAAGGTCAGCATTT 1

RESULT 11

AAZ23794/c

ID AAZ23794 standard; DNA; 24 BP.

XX AAZ23794;

XX 07-MAR-2002 (first entry)

DE Rat prostatic adenocarcinoma cell cDNA amplifying Tbetals reverse primer.

XX Rat; thymosin betal5 protein; G-actin; cell motility; therapy;

KW prostate cancer; cytosstatic; reverse transcription; RT; PCR primer; ss.

XX Rattus sp.

OS US6300479-B1.

XX 09-OCT-2001.

XX 06-AUG-1999; 99US-00369744.

XX 17-JUN-1996; 96US-00664856.

PR 14-FEB-1997; 97US-00801796.

PR 17-SEP-1997; 97US-00931877.

PR 29-APR-1998; 98US-00069484.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Zetter BR, Bao L;

XX WPI; 2002-033180/04.

XX An antibody which selectively binds to a thymosin betal5 protein is
 PT useful to detect, prevent or treat cancer, particularly of the prostate.

XX Example; Col 12; 22pp; English.

XX The invention relates to nucleic acids encoding human thymosin betal5
 CC protein, that has the ability to bind and sequester G-actin and directly
 CC regulates cell motility in prostatic carcinoma cells. The antibodies of
 CC thymosin betal5 protein may be used to diagnose, treat or prevent cancer
 CC particularly prostate cancer. The present sequence is a reverse
 CC transcription (RT)-PCR primer used to amplify rat prostatic
 CC adenocarcinoma cell cDNA. This sequence is used in the exemplification of
 CC the invention

XX Sequence 24 BP; 6 A; 5 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 5.8%; Score 24; DB 6; Length 24;

Best Local Similarity 100.0%; Pred. No. 6.6e+03;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 ACCCTGACTGAAGGTCAGCATTT 379
 |||||
 DB 24 ACCCTGACTGAAGGTCAGCATTT 1

RESULT 12

AAZ23793

ID AAZ23793 standard; DNA; 24 BP.

XX AAZ23793;

XX 07-MAR-2002 (first entry)

DE Rat prostatic adenocarcinoma cell cDNA amplifying Tbetals forward primer.

XX Rat; thymosin betal5 protein; G-actin; cell motility; therapy;

KW prostate cancer; cytostatic; reverse transcription; RT; PCR primer; ss.
XX Rattus sp.
XX US6300479-B1.
XX 09-OCT-2001.
XX 06-AUG-1999; 99US-00369744.
XX 17-JUN-1996; 96US-00664856.
PR 14-FEB-1997; 97US-00801796.
PR 17-SEP-1997; 97US-00931877.
PR 29-APR-1998; 98US-00069484.
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX Zetter BR, Bao L;
XX WPI; 2002-033180/04.
XX An antibody which selectively binds to a thymosin beta15 protein is
PT useful to detect, prevent or treat cancer, particularly of the prostate.
XX Example; Col 12; 22pp; English.
XX The invention relates to nucleic acids encoding human thymosin beta15
CC protein, that has the ability to bind and sequester G-actin and directly
CC regulates cell motility in prostatic carcinoma cells. The antibodies of
CC thymosin beta15 protein may be used to diagnose, treat or prevent cancer
CC particularly prostate cancer. The present sequence is a reverse
CC transcription (RT)-PCR primer used to amplify rat prostatic
CC adenocarcinoma cell cDNA. This sequence is used in the exemplification of
CC the invention
XX
SQ Sequence 24 BP; 4 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
Query Match 5.8%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TATCAGCTAGTGGCTGCACCCGCG 24
Db 1 TATCAGCTAGTGGCTGCACCCGCG 24
RESULT 13
ADF61760/c
ID ADF61760 standard; DNA; 24 BP.
XX ADF61760;
XX 12-FEB-2004 (revised)
DT 29-JAN-2004 (first entry)
XX Rat thymosin beta-15 RT-PCR primer, SEQ ID NO:9.
XX Human; rat; thymosin beta-15; G-actin sequestration;
KW cell motility regulation; neoplastic cell; prostatic carcinoma;
KW prostate cancer; lung cancer; melanoma; breast cancer; metastatic cancer;
KW diagnosis; prognosis; antisense therapy; gene therapy; cytostatic;
KW thymosin beta-15 antagonist; adenocarcinoma RNA;
KW reverse transcription-PCR; RT-PCR; primer; ss.
XX Rattus sp.
OS
XX US2002183496-A1.
FN
XX 05-DEC-2002.
PD
XX 05-JUN-2001; 2001US-00874736.
PF
XX 17-JUN-1996; 96US-00664856.
PR

PR 14-FEB-1997; 97US-00801796.
PR 17-SEP-1997; 97US-00931877.
PR 29-APR-1998; 98US-00069484.
PR 06-AUG-1999; 99US-00369744.
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX Zetter BR, Bao L;
XX WPI; 2004-040942/04.
XX New isolated polynucleotide encoding human thymosin beta15 for diagnosing
PT and prognosing particular cancers, especially metastatic cancers.
XX Example; SEQ ID NO 9; 23pp; English.
XX The invention relates to human thymosin beta-15 (ADF61753) and cDNA
CC encoding it (ADF61752). The invention also relates to recombinant vectors
CC and host cells comprising human thymosin beta-15 nucleic acids,
CC antibodies which specifically bind human thymosin beta-15,
CC oligonucleotides at least 10 nucleotides in length which hybridise to
CC human thymosin beta-15 cDNA, and methods of treating neoplastic cells
CC expressing thymosin beta-15. Like other members of the thymosin beta
CC family, thymosin beta-15 has the ability to bind and sequester G-actin,
CC but unlike other beta thymosins, it also directly regulates cell motility
CC in prostatic carcinoma cells. Additionally, enhanced expression of
CC thymosin beta-15 in non-testicular cells has a high correlation to
CC disease state in a number of cancers, such as prostate, lung, melanoma
CC and breast cancer, particularly metastatic cancers. Human thymosin beta-
CC 15 nucleic acids can therefore be used in the diagnosis and prognosis of
CC various cancers, especially metastatic cancers. Cancers which express
CC thymosin beta-15 may be treated by suppressing the activity or expression
CC of thymosin beta-15, for example by administering thymosin beta-15
CC antisense oligonucleotides or thymosin beta-15-specific antibodies. The
CC present sequence is related to the invention.
XX
SQ Sequence 24 BP; 6 A; 5 C; 6 G; 7 T; 0 U; 0 Other;
Query Match 5.8%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 356 ACCCTGACTGAAGGTCAGCATTT 379
Db 24 ACCCTGACTGAAGGTCAGCATTT 1
RESULT 14
ADF61759
ID ADF61759 standard; DNA; 24 BP.
XX ADF61759;
XX 12-FEB-2004 (revised)
DT 29-JAN-2004 (first entry)
XX Rat thymosin beta-15 RT-PCR primer, SEQ ID NO:8.
XX Human; rat; thymosin beta-15; G-actin sequestration;
KW cell motility regulation; neoplastic cell; prostatic carcinoma;
KW prostate cancer; lung cancer; melanoma; breast cancer; metastatic cancer;
KW diagnosis; prognosis; antisense therapy; gene therapy; cytostatic;
KW thymosin beta-15 antagonist; adenocarcinoma RNA;
KW reverse transcription-PCR; RT-PCR; primer; ss.
XX Rattus sp.
OS
XX US2002183496-A1.
FN
XX 05-DEC-2002.
PD
XX 05-JUN-2001; 2001US-00874736.
PF
XX

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PR 17-JUN-1996; 96US-00664856.
PR 14-FEB-1997; 97US-00801796.
PR 17-SEP-1997; 97US-00931877.
PR 29-APR-1998; 98US-00069484.
PR 06-AUG-1999; 99US-00369744.
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX PA
XX Zetter BR, Bao L;
XX WPI; 2004-040942/04.
DR WPI; 2004-040942/04.
XX
XX New isolated polynucleotide encoding human thymosin beta15 for diagnosing
XX and prognosing particular cancers, especially metastatic cancers.
XX
XX Example; SEQ ID NO 8; 23pp; English.
PS
XX The invention relates to human thymosin beta-15 (ADF61753) and cDNA
XX encoding it (ADF61752). The invention also relates to recombinant vectors
XX and host cells comprising human thymosin beta-15 nucleic acids,
XX antibodies which specifically bind human thymosin beta-15,
XX oligonucleotides at least 10 nucleotides in length which hybridise to
XX human thymosin beta-15 cDNA, and methods of treating neoplastic cells
XX expressing thymosin beta-15. Like other members of the thymosin beta
XX family, thymosin beta-15 has the ability to bind and sequester G-actin,
XX but unlike other beta thymosins, it also directly regulates cell motility
XX in prostatic carcinoma cells. Additionally, enhanced expression of
XX thymosin beta-15 in non-testicular cells has a high correlation to
XX disease state in a number of cancers, such as prostate, lung, melanoma
XX and breast cancer, particularly metastatic cancers. Human thymosin beta-
XX 15 nucleic acids can therefore be used in the diagnosis and prognosis of
XX various cancers, especially metastatic cancers. Cancers which express
XX thymosin beta-15 may be treated by suppressing the activity or expression
XX of thymosin beta-15, for example by administering thymosin beta-15
XX antisense oligonucleotides or thymosin beta-15-specific antibodies. The
XX present sequence is related to the invention.
XX
XX Sequence 24 BP; 4 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
SQ
Query Match 5.8%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATCAGCTAGTGGCTGCACCCGCG 24
DB 1 TATCAGCTAGTGGCTGCACCCGCG 24
RESULT 15
ADP44092
ID ADP44092 standard; DNA; 24 BP.
XX
XX ADP44092;
XX
XX 12-AUG-2004 (first entry)
XX Human thymosin beta-15 cDNA RT-PCR primer #1.
XX
XX Human thymosin beta-15; RT-PCR; ss; cancer; prostate; lung; melanoma;
XX breast; cytosstatic; primer; reverse transcriptase.
XX
XX Homo sapiens.
XX
XX US2004101910-A1.
XX
XX 27-MAY-2004.
XX
XX 03-DEC-2003; 2003US-00726422.
XX
XX 17-JUN-1996; 96US-00664856.
XX 14-FEB-1997; 97US-00801796.
XX 17-SEP-1997; 97US-00931877.
XX 29-APR-1998; 98US-00069484.
XX 06-AUG-1999; 99US-00369744.
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX PA
XX Zetter BR, Bao L;
XX WPI; 2004-459889/43.
DR WPI; 2004-459889/43.
XX
XX Novel isolated and purified human thymosin beta15, useful for diagnosing
XX cancers such as prostate, lung, melanoma and breast cancer, particularly
XX metastatic cancers.
XX
XX Example; SEQ ID NO 8; 23pp; English.
PS
XX The invention relates to the human thymosin beta-15 polypeptide and the
XX polynucleotide encoding it. The invention also relates to an antibody
XX that selectively binds human thymosin beta-15 and a method of treating a
XX neoplastic cell expressing human thymosin beta-15 by administering to the
XX cell a compound which suppresses the activity or production of human
XX thymosin beta-15. The antibody is useful for treating a neoplastic cell
XX expressing human thymosin beta-15. The polypeptide and antibody are
XX useful for treating, diagnosing or preventing cancers such as prostate
XX cancer, lung cancer, melanoma and breast cancer, particularly metastatic
XX cancers, where enhanced transcripts (mRNA) and expression of the thymosin
XX beta-15 gene in non-testicular cells have a high correlation to disease
XX state in the cancers. (ii) is useful for treating or preventing cancers.
XX This sequence represents a reverse transcriptase PCR (RT-PCR) primer used
XX to amplify cDNA encoding the human thymosin beta-15 polypeptide of the
XX invention.
XX
XX Sequence 24 BP; 4 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
SQ
Query Match 5.8%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATCAGCTAGTGGCTGCACCCGCG 24
DB 1 TATCAGCTAGTGGCTGCACCCGCG 24
Search completed: March 12, 2006, 07:36:09
Job time : 486 secs

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OM nucleic - nucleic search, using sw model

Run on: March 12, 2006, 05:37:06 ; Search time 3628 Seconds
(without alignments)
5313.197 Million cell updates/sec

Title: US-10-726-422-1
Perfect score: 412
Sequence: 1 FATCAGCTAGTGGTCGACC.....AAATGCTTTTCCACTGCTC 412

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 105260
Minimum DB seq length: 10
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gsa1:*
10: gb_gsa2:*
11: gb_gsa3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	19.4	4.7	38	11 CR399055	CR399055 Arabidops
C 2	19	4.6	36	9 BH812364	BH812364 SALK 0616
C 3	18.8	4.6	39	1 AW247125	AW247125 281975.3
C 4	18.6	4.5	33	9 AZ311457	AZ311457 IM0026121
C 5	18.6	4.5	39	10 C2914406	C2914406 4013006G1
C 6	18.2	4.4	35	9 AZ450518	AZ450518 IM0249J13
C 7	18	4.4	37	10 AL952209	AL952209 Arabidops
C 8	18	4.4	39	10 C2467113	C2467113 C01377-5p
C 9	18	4.4	40	1 A1185980	A1185980 q34c06.8
C 10	17.8	4.3	31	1 AA912393	AA912393 OL99C01.8
C 11	17.8	4.3	37	1 A1181597	A1181597 uc63d11.r
C 12	17.6	4.3	38	10 C2490399	C2490399 f07663-3p
C 13	17.6	4.3	38	10 AJ593144	AJ593144 Arabidops
C 14	17.4	4.2	36	8 D19985	D19985 HUMGS00952
C 15	17.4	4.2	39	1 AB088497	AB088497 AB088497
C 16	17.2	4.2	34	1 AA624893	AA624893 vn83h01.r
C 17	17.2	4.2	36	8 D21040	D21040 HUMGS02024
C 18	17.2	4.2	38	5 BW593340	BW593340 BW593340
C 19	17.2	4.2	40	9 BZ288540	BZ288540 SALK 0219
C 20	17	4.1	34	3 BJ066456	BJ066456 BJ066456
C 21	17	4.1	36	10 AJ600605	AJ600605 Arabidops
C 22	17	4.1	39	7 C0777934	C0777934 BL002B_H1

23	16.8	4.1	31	1 AU254837	AU254837
24	16.8	4.1	34	9 BH901287	BH901287 SALK_0742
25	16.8	4.1	36	6 CF301054	CF301054 TLEAF-05
C 26	16.8	4.1	36	10 AJ595967	AJ595967 Arabidops
C 27	16.8	4.1	36	10 CG725443	CG725443 1119085D0
C 28	16.8	4.1	38	10 C2475333	C2475333 d06763-5p
C 29	16.8	4.1	40	9 BH846939	BH846939 SALK 0120
C 30	16.6	4.0	30	9 AZ312821	AZ312821 IM0038C18
C 31	16.6	4.0	36	10 CL528781	CL528781 HIV69G09.
C 32	16.6	4.0	37	1 AA947987	AA947987 OQ58602.8
C 33	16.6	4.0	37	10 C2466979	C2466979 C01204-3p
C 34	16.6	4.0	39	1 AW246452	AW246452 2821649.3
C 35	16.6	4.0	40	1 A1022013	A1022013 ow64C01.x
C 36	16.4	4.0	34	1 A1958680	A1958680 fc95801.y
C 37	16.4	4.0	34	9 BZ290649	BZ290649 SALK 0908
C 38	16.4	4.0	37	1 A1587823	A1587823 AL587823
C 39	16.4	4.0	39	9 BZ762643	BZ762643 SALK 1060
C 40	16.2	3.9	32	9 AZ313810	AZ313810 IM0030K16
C 41	16.2	3.9	32	10 AL755578	AL755578 Arabidops
C 42	16.2	3.9	34	9 AZ979561	AZ979561 2M0256J15
C 43	16.2	3.9	34	9 BZ290649	BZ290649 SALK 0908
C 44	16.2	3.9	34	11 TA28804Q	AL453260 T. brucei
C 45	16.2	3.9	35	9 AZ980857	AZ980857 2M0258L05

ALIGNMENTS

RESULT 1	CR399055/c	38 bp	DNA	linear	GSS 02-MAY-2004
LOCUS	CR399055/c	38 bp	DNA	linear	GSS 02-MAY-2004
DEFINITION	Arabidopsis thaliana T-DNA flanking sequence GK-814F03-025642,				
ACCESSION	CR399055				
VERSION	CR399055.1				
KEYWORDS	GSS				
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
REFERENCE	Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P., and Weisshaar, B.				
AUTHORS	GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana				
JOURNAL	Bioinformatics 19 (11), 1441-1442 (2003)				
PUBMED	12874060				
REFERENCE	2				
AUTHORS	Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.				
TITLE	An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics				
JOURNAL	Plant Mol. Biol. 53 (1-2), 247-259 (2003)				
PUBMED	14756321				
REFERENCE	3				
AUTHORS	Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and Weisshaar, B.				
TITLE	High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines				
JOURNAL	Bioinformatics 19 (11), 1441-1442 (2003)				
PUBMED	14682050				
REFERENCE	4				
AUTHORS	Strizhov, N., Li, Y., Rosso, M.G. and Weisshaar, B.				
TITLE	Direct Submission				
JOURNAL	Submitted (01-MAY-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany				
COMMENT	This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At1g48790. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated				

'GABI'. Information on line availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES

source
1..38
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-814F03-025642"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC106 (GenBank accession number: AJ537513). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 4.7%; Score 19.4; DB 11; Length 38;
Best Local Similarity 70.3%; Pred. No. 2e+06; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 11;

QY 101 AGTGATAACCCAGACTTATCAGAAGTTGAACATTGG 137

Db 38 AGCGAAAGTCCAGAAGTATCAGAATGAATTTATTG 2

RESULT 2

BH812364/c
LOCUS BH812364 36 bp DNA linear GSS 02-MAY-2002
DEFINITION SALK 061675 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_061675, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

REFERENCE

AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

TITLE

JOURNAL

COMMENT

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@alk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within an annotated exon of At4g25330.

Class: TDNA tagged.

FEATURES

source

1..36
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_061675"
/note="PCR was performed on Arabidopsis thaliana TDNA insertion lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 4.6%; Score 19; DB 9; Length 36;
Best Local Similarity 71.4%; Pred. No. 2.5e+06;
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 242 ATTCTCTCTCAAGAGCAACTTCAACTTTGCTGGA 276

Db 35 ATTCTGCTATTCAAAACAACITTAAGCGTTGATGGA 1

RESULT 3

AW247125/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other_ESRs: 2819775.5prime

Contact: Robert Strausberg, Ph.D.

Email: csgbbs-remail.nih.gov

Tissue Procurement: DCTD/BTP CDNA Library Preparation: Ling

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing

project Clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LLNL at:

http://www.llnl.gov/bbrp/image/image.html Base Calling / Quality

Scores: PHRED from University of Washington Genome Center

Trimming: cross match from University of Washington Genome Center

PhRAP suite. Poly-T Identification: patMatch.pl from Berkeley

Drosophila Genome Project. University of Washington Genome Center:

http://www.genome.washington.edu Low Quality Sequence: 13

contiguous PHRED high quality bases following vector sequence. Very

Low Quality Sequence: Trace file contained 39 contiguous distinct

peaks following vector sequence. Polyadenylation: Based upon the

presence of a XhoI site followed by a run of 14 or more T residues

at the beginning of the sequence, this cDNA insert was

polyadenylated.

Plate: L1CM2 row: H column: 16

High quality sequence stop: 13.

Location/Qualifiers

1..39

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clones="IMAGE:2819775"

/tissue_type="small cell carcinoma"

/cell_lines="MGC3"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_7"

/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 4.6%; Score 18.8; DB 1; Length 39;
Best Local Similarity 68.4%; Pred. No. 2.9e+06;
Matches 26; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Genomic survey sequence.
 CZ467113
 VERSION CZ467113.1 GI:62961126
 GSS
 KEYWORDS
 SOURCE
 ORGANISM
 Drosophila melanogaster (fruit fly)
 Drosophila melanogaster
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
 1 (bases 1 to 39)
 Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A.,
 Singh, C.M., Buchholz, R., Densky, M., Fawcett, R., Francis-Lang, H.L.,
 Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W.,
 Greer, K., Hartouni, S.R., Howie, E., Jakkula, L., Joo, D., Killpack, K.,
 Laufer, A., Mazzotta, J., Smith, R.D., Stevens, L.M., Stuber, C.,
 Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, F.,
 Swimmer, C., Kopczyński, C., Duyk, G., Winberg, M.L. and Margolis, J.
 A complementary transposon tool kit for Drosophila melanogaster
 using P and piggyBac
 Nat. Genet. 36 (3), 283-287 (2004)

TITLE
 A complementary transposon tool kit for Drosophila melanogaster
 using P and piggyBac
 14981521
 JOURNAL
 PUBMED
 COMMENT

CONTACT: Roger A Hoskins
 Berkeley Drosophila Genome Project
 Lawrence Berkeley National Laboratory
 Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
 Tel: 510 486 4015
 Fax: 510 486 6798
 Email: RHoskins@lbl.gov
 Sequence recovery method was inverse PCR.
 Sequence orientation is forward strand relative to 5' end of
 piggyBac element.
 The piggyBac insertion position is 36 in the 39 bases. This
 insertion position refers to the first base of the 4 base TTTAA
 target recognition sequence.
 Class: transposon insertion site.
 Location/Qualifiers
 1..39
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /strain="isogenic w- strain"
 /db_xref="taxon:7227"
 /clone_lib="Exelixis piggyBac PB insertions"
 /note="Vector: piggyBac PB (GenBank accession number
 AY515146); An isogenic w- Drosophila melanogaster strain
 was mutagenized by remobilization of transposable
 elements. We remobilized the PB element using
 Hsp70:piggyBac transposase from a single amnion
 element on either the X or third chromosome. We induced
 transposase expression by immersing bottles in a
 circulating 37°C water bath for a daily (days 3-10 after
 egg-laying) 1-h heat shock. We outcrossed the resulting
 dysgenic males to an isogenic w- strain. New insertions
 were identified on the basis of a change in eye color
 (third chromosome amnion) or the appearance of w+ male
 progeny (X chromosome amnion). All lines were mapped
 to a chromosome by standard genetic methods, examined for
 homozygous viability, and used for recovery of flanking
 genomic sequence by inverse PCR."

ORIGIN
 Query Match 4.4%; Score 18; DB 10; Length 39;
 Best Local Similarity 70.6%; Pred. No. 4.8e+06;
 Matches 24; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 211 GAAGAATATATCAAGATCATTAATGAGATT 244
 |||||
 DB 4 GAAGAATAAAGCAAGAAAGAAAAATACAAATT 37
 |||||

RESULT 9
 A1185980/c 40 bp mRNA linear EST 29-OCT-1998
 LOCUS qe34c06.s1 Soares_fetal_lung_NBHL19W Homo sapiens cDNA clone
 DEFINITION

IMAGE:1740874 3' similar to TR:Q33574 Q33574 ORF2 BASIS 1807-2850.
 ;, mRNA sequence.
 A1185980
 VERSION A1185980.1 GI:3736618
 EST
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 1 (bases 1 to 40)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Trace considered overall poor quality
 Insert Length: 1355 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1..40
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1740874"
 /dev_stage="19 weeks"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares fetal lung NBHL19W"
 /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer
 [5'-TGTTACCAATCTGAAGTGGAGCGCGCAATTTTCTTTT-3']
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT7T3 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M. Fatima Bonaldo. This library was constructed
 from the same fetus as the fetal heart library, Soares
 fetal heart NBHL19W."

ORIGIN
 Query Match 4.4%; Score 18; DB 1; Length 40;
 Best Local Similarity 70.6%; Pred. No. 4.8e+06;
 Matches 24; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 190 GAAGGAATCTCCAGCAGGAGAGAAATATAAT 223
 |||||
 DB 34 GAAGTAAATATTAACATATAGAAATAGAT 1
 |||||

RESULT 10
 AA912393
 LOCUS
 DEFINITION
 AA912393 31 bp mRNA linear EST 10-JUN-1998
 similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;, mRNA
 sequence.
 AA912393
 VERSION AA912393.1 GI:3051785
 EST
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 1 (bases 1 to 31)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL
COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
unknown library type

Insert Length: 720 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES
source

Location/Qualifiers
1..31
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1537728"
/tissue_type="dorsal root ganglion"
/lab_host="DH10B"
/clone_lib="NCI-CCAP_PNS1"
/note="Organ: peripheral nervous system; Vector:
pCMV-SPORT4; Site 1: SalI; Site 2: NotI; Cloned
unidirectionally. - Primer: Oligo dt. Average insert size
1.1 kb."

ORIGIN

Query Match 4.3%; Score 17.8; DB 1; Length 31;
Best Local Similarity 75.9%; Pred. No. 5.2e+06;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 278 AGCTTGGATTAGACATGTTCTGTAA 306
Db 2 AGCCAGGTACTTAAACTGTTCTGTAA 30

RESULT 11
LOCUS

A1181597 A1181597 37 bp mRNA linear EST 08-OCT-1998
DEFINITION uc63dl1.r1 Soares_mammary_gland_NBMGM Mus musculus cDNA clone
IMAGE:1430325 5' similar to SW:ClB_HUMAN Q99828 SNK INTERACTING
PROTEIN 2-28 ;, mRNA sequence.

ACCESSION
VERSION

A1181597 GI:3732235
EST.

KEYWORDS
SOURCE

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 37)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,P., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.

The WashU-HMI Mouse EST Project
Unpublished (1996)

JOURNAL
COMMENT

Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:914393

Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.

FEATURES
source

Location/Qualifiers
1..37
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"

/clone="IMAGE:1430325"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"

/clone_lib="Soares_mammary_gland_NBMGM"
/note="Organ: mammary gland; Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dt) primer [5'
TGTTCAATCTGAAGTGGAGCGCGCGAATGTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M. Fatima
Bonaldo."

ORIGIN

Query Match 4.3%; Score 17.8; DB 1; Length 37;
Best Local Similarity 67.6%; Pred. No. 5.4e+06;
Matches 25; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy 41 GGAGTAGCTCGGACAGAATTGCTGGCTAGTAGAAG 77
Db 1 GCAGTCGCTGTCTAAGGAGCTGCTGCCGAGTACCAG 37

RESULT 12
LOCUS

CZ490399 CZ490399 38 bp DNA linear GSS 29-APR-2005
DEFINITION f07663-3prime Exelixis piggyBac WH insertions Drosophila
melanogaster genomic sequence recovered from 3' end of piggyBac,
genomic survey sequence.

ACCESSION
VERSION

CZ490399 GI:62987837

KEYWORDS
SOURCE

GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
AUTHORS

1 (bases 1 to 38)
Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A.,
Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L.,
Ryner,L., Cheung,J.M., Chong,A., Erickson,C., Fieher,W.W.,
Greer,K., Hartouni,S.R., Howie,E., Jakkula,L., Joo,D., Killpack,K.,
Laufer,A., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C.,
Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F.,
Swimmer,C., Kopczyński,C., Duyk,G., Winberg,M.L. and Margolis,J.
A complementary transposon tool kit for Drosophila melanogaster
using P and piggyBac

JOURNAL
PUBMED

Nat. Genet. 36 (3), 283-287 (2004)
14981521
Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798

Email: RHoskins@lbl.gov
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of
piggyBac element.

The piggyBac insertion position is 1 in the 38 bases. This
insertion position refers to the first base of the 4 base TTTAA
target recognition sequence.

Class: transposon insertion site.
Location/Qualifiers

1..38
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="isogenic w- strain"

```

/db_xref="taxon:7227"
/clone_lib="Exelixis piggyBac WH insertions"
/Note="Vector: piggyBac WH (GenBank accession number
AY515148); An isogenic w- Drosophila melanogaster strain
was mutagenized by remobilization of transposable
elements. We remobilized the WH element using the
constitutive alpha-1 tubulin: piggyBac transposase source.
We remobilized the WH element from a single ammunition
element on the Binsency balancer chromosome in dysgenic
females. We outcrossed dysgenic virgin females in vials to
the isogenic w- strain and selected new hops in the
following generation. All lines were mapped to a
chromosome by standard genetic methods, examined for
homozygous viability, and used for recovery of flanking
genomic sequence by inverse PCR."

ORIGIN
Query Match 4.3%; Score 17.6; DB 10; Length 38;
Best Local Similarity 71.9%; Pred. No. 6.1e+06;
Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 317 ATGTAGACATTTAGCGGTTCTCGATAGGTT 348
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4 ATATTGATTTTCAGGTGGTTCGGATTGAT 35

RESULT 13
AJ5931144/c
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
375609, genomic survey sequence.
38 bp DNA linear GSS 15-JAN-2004
AJ5931144
ACCESSION
VERSION
AJ593114.1 GI:37942768
KEYWORDS
GSS; left border; T-DNA flanking sequence.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
1
AUTHORS
Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepiniec, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED
12446565
2 (bases 1 to 38)
Balzergue, S.
Direct Submission
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'genoplatte' (http://www.genoplatte.com and
http://genoplatte-info.infobiogen.fr).

FEATURES
Location/Qualifiers
1..38
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone_lib="375G09"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Wassilewskija"

misc_feature
1..38
/note="T-DNA flanking sequence

```

```

left border"

ORIGIN
Query Match 4.3%; Score 17.6; DB 10; Length 38;
Best Local Similarity 71.9%; Pred. No. 6.1e+06;
Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 212 AAGAATATATCAAGATCATATAAATGAGAT 243
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32 AATAAGAAAAATAAAGATCATATAAATTTGAT 1

RESULT 14
D19985
LOCUS
DEFINITION
HUMGS00952 Human promyelocyte Homo sapiens cDNA clone mm3314 3',
mRNA sequence.
36 bp mRNA linear EST 30-JUL-1996
D19985
ACCESSION
VERSION
D19985.1 GI:500882
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 36)
AUTHORS
Okubo, K., Fukushima, A., Yoshii, J., Niiyama, T., Kojima, Y.,
Yoshinari, H., Arimoto, J. and Matsubara, K.
Gene expression of human promyelocytic cell line HL60 before and
after induction of differentiation. A new application of 3'directed
cDNA sequencing
Unpublished (1993)
JOURNAL
COMMENT
Contact: Okubo, K., Fukushima, A., Yoshii, J., Niiyama, T., Kojima, Y.,
Yoshinari, H., Arimoto, J. and Matsubara, K.
Institute for Molecular and Cellular Biology
Osaka University
3-1 Yamada-oka, Suita, Osaka 565, Japan.

FEATURES
Location/Qualifiers
1..36
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="mm3314"
/clone_lib="Human promyelocyte"
/note="Female, adult, cell_line = HL60, cell_type =
promyelocyte."

ORIGIN
Query Match 4.2%; Score 17.4; DB 8; Length 36;
Best Local Similarity 77.8%; Pred. No. 6.9e+06;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 121 AGAAGTCGAACATTTGACAAATCAA 147
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 10 AGAAAAATAAATAATTTAAAAATCAA 36

RESULT 15
AB088497
LOCUS
DEFINITION
AB088497 lambda Triplex2 rice phloem sap cDNA Oryza sativa
(japonica cultivar-group) cDNA clone PA426, mRNA sequence.
ACCESSION
VERSION
AB088497.1 GI:28298596
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 39)
AUTHORS
Mano, H., Noguchi, M., Oshima, T., Yoneyama, T., Hayaishi, H. and
Fujiwara, T.

```

TITLE Small RNAs detected in the rice phloem sap
JOURNAL Unpublished (2003)
COMMENT Contact: Hironori Mano
Plant Genome Center Co., Ltd
Kannondail-25-2, Tsukuba, Ibaraki 305-0856, Japan
Tel: 81-298-39-4823
Email: hmano@gcdna.co.jp.

FEATURES
SOURCE Location/Qualifiers
1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="PA426"
/tissue_type="phloem"
/clone_lib="lambda Triplex2 rice phloem sap cDNA"

ORIGIN

Query Match 4.2%; Score 17.4; DB 1; Length 39;
Best Local Similarity 77.8%; Pred No. 7e+06;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 214 AGAATATATCAAGATCATATAAATGA 240
| | | | | | | | | | | | | | | | | | | | |
Db 5 AAAATATATCTCCATATGATATATGA 31

Search completed: March 12, 2006, 06:44:17
Job time : 3632 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 12, 2006, 05:43:55 ; Search time 794 Seconds
(without alignments)
4290.912 Million cell updates/sec

Title: US-10-726-422-1

Perfect score: 412

Sequence: 1 TATCAGCTAGGCTGCACCC.....AAATGTTTTCCTACTGCTC 412

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134699005 residues

Total number of hits satisfying chosen parameters: 10877748

Minimum DB seq length: 10

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.Main.*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	6.1	25	7 US-10-719-956-99595	Sequence 99595, A
2	25	6.1	25	7 US-10-719-956-151661	Sequence 151661, A
3	25	6.1	25	7 US-10-719-956-200130	Sequence 200130, A
4	25	6.1	25	7 US-10-719-956-283879	Sequence 283879, A
5	25	6.1	25	7 US-10-719-956-302980	Sequence 302980, A
6	25	6.1	25	7 US-10-719-956-338333	Sequence 338333, A
7	25	6.1	25	7 US-10-719-956-533192	Sequence 533192, A
8	25	6.1	25	7 US-10-719-956-559423	Sequence 559423, A
9	25	6.1	25	7 US-10-719-956-560901	Sequence 560901, A
10	25	6.1	25	7 US-10-719-956-582115	Sequence 582115, A
11	25	6.1	25	7 US-10-719-956-589182	Sequence 589182, A
12	24	5.8	24	3 US-09-874-736-9	Sequence 8, Appli
13	24	5.8	24	3 US-09-874-736-9	Sequence 9, Appli
14	24	5.8	24	7 US-10-726-422-8	Sequence 8, Appli
15	24	5.8	24	7 US-10-726-422-9	Sequence 9, Appli
16	23.4	5.7	25	7 US-10-719-956-99596	Sequence 99596, A
17	23.4	5.7	25	7 US-10-719-956-151662	Sequence 151662, A
18	23.4	5.7	25	7 US-10-719-956-200127	Sequence 200127, A
19	23.4	5.7	25	7 US-10-719-956-283880	Sequence 283880, A
20	23.4	5.7	25	7 US-10-719-956-302981	Sequence 302981, A
21	23.4	5.7	25	7 US-10-719-956-338332	Sequence 338332, A
22	23.4	5.7	25	7 US-10-719-956-533193	Sequence 533193, A
23	23.4	5.7	25	7 US-10-719-956-559422	Sequence 559422, A

24 23.4 5.7 25 7 US-10-719-956-560900 Sequence 560900, A
25 23.4 5.7 25 7 US-10-719-956-562114 Sequence 562114, A
26 23.4 5.7 25 7 US-10-719-956-589183 Sequence 589183, A
27 23.4 5.7 25 8 US-10-719-900-767247 Sequence 767247, A
28 23.4 5.7 25 10 US-11-036-317-97871 Sequence 97871, A
29 22.4 5.4 25 10 US-11-036-317-81339 Sequence 81339, A
30 21.8 5.3 25 8 US-10-719-900-767246 Sequence 767246, A
31 21.8 5.3 25 10 US-11-036-317-90714 Sequence 90714, A
32 21.8 5.3 25 10 US-11-036-317-363388 Sequence 363388, A
33 21.8 5.3 25 10 US-11-036-317-391064 Sequence 391064, A
34 20.8 5.0 25 8 US-10-719-900-851769 Sequence 851769, A
35 20.8 5.0 25 8 US-10-719-900-851770 Sequence 851770, A
36 20.8 5.0 25 10 US-11-036-317-339568 Sequence 339568, A
37 20.8 5.0 25 10 US-11-036-317-361725 Sequence 361725, A
c 38 20.4 5.0 36 7 US-10-179-940-374 Sequence 374, Appl
39 20.2 4.9 25 7 US-10-029-020-90 Sequence 90, Appl
40 20.2 4.9 25 8 US-10-719-900-739286 Sequence 739286, A
41 20.2 4.9 25 10 US-11-036-317-249261 Sequence 249261, A
42 20.2 4.9 25 10 US-11-036-317-262889 Sequence 262889, A
43 19.6 4.8 40 3 US-09-874-931C-450 Sequence 450, Appl
c 44 19.4 4.7 33 9 US-10-492-928A-71 Sequence 71, Appl
c 45 19.4 4.7 40 7 US-10-416-249-588 Sequence 588, Appl

ALIGNMENTS

RESULT 1
US-10-719-956-99595
; Sequence 99595, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 99595
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-99595

Query Match 6.1%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 ACTTCAACTTTGCTGGATAGTCTTG 284
|||||
DB 1 ACTTCAACTTTGCTGGATAGTCTTG 25

RESULT 2
US-10-719-956-151661
; Sequence 151661, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 151661
; LENGTH: 25
; TYPE: DNA

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; ORGANISM: Rattus norvegicus
US-10-719-956-151661

Query Match
Best Local Similarity 6.1%; Score 25; DB 7; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 368 AGGTCAGCATTTAACACCAATCAATT 392
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Db 1 AGGTCAGCATTTAACACCAATCAATT 25

RESULT 3
US-10-719-956-200130
; Sequence 200130, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 200130
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-200130

Query Match
Best Local Similarity 6.1%; Score 25; DB 7; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 317 ATGTAGACATTTTAGCGGTTCTCTG 341
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Db 1 ATGTAGACATTTTAGCGGTTCTCTG 25

RESULT 4
US-10-719-956-283879
; Sequence 283879, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 283879
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-283879

Query Match
Best Local Similarity 6.1%; Score 25; DB 7; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 170 GAAAGAATACTCTTCTTCGAAGG 194
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Db 1 GAAAGAATACTCTTCTTCGAAGG 25

RESULT 5
US-10-719-956-302980
; Sequence 302980, Application US/10719956
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; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 302980
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-302980

Query Match
Best Local Similarity 6.1%; Score 25; DB 7; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 GAAGCTTTGGAACGAGCAGTCAAGA 98
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Db 1 GAAGCTTTGGAACGAGCAGTCAAGA 25

RESULT 6
US-10-719-956-338333
; Sequence 338333, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 338333
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-338333

Query Match
Best Local Similarity 6.1%; Score 25; DB 7; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 239 GAGATTCTCTCTCAAGAGCAACTT 263
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Db 1 GAGATTCTCTCTCAAGAGCAACTT 25

RESULT 7
US-10-719-956-533192
; Sequence 533192, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 533192
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
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US-10-719-956-533192
Query Match          6.1%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 GTTCTGTAAACCTTCAATATGT 320
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Db 1 GTTCTGTAAACCTTCAATATGT 25

RESULT 8
US-10-719-956-559423
; Sequence 559423, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 559423
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-559423

Query Match          6.1%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 TAGCTGCGGACAGAAATGCTGCCT 69
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Db 1 TAGCTGCGGACAGAAATGCTGCCT 25

RESULT 9
US-10-719-956-560901
; Sequence 560901, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 560901
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-560901

Query Match          6.1%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 329 TAGCGGTTTCCTGATAGTTCCTAA 353
      |||||
Db 1 TAGCGGTTTCCTGATAGTTCCTAA 25

RESULT 10
US-10-719-956-562115
; Sequence 562115, Application US/10719956
; Publication No. US20040146910A1
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; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 562115
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-562115

Query Match          6.1%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 TAGGTTCTTAAGTACCCCTGACTGAA 367
      |||||
Db 1 TAGGTTCTTAAGTACCCCTGACTGAA 25

RESULT 11
US-10-719-956-589182
; Sequence 589182, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 589182
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-589182

Query Match          6.1%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 184 TCCTTCGAAGGAAGAACTATCCAGCAG 208
      |||||
Db 1 TCCTTCGAAGGAAGAACTATCCAGCAG 25

RESULT 12
US-09-874-736-8
; Sequence 8, Application US/09874736
; Publication No. US20020183496A1
; GENERAL INFORMATION:
; APPLICANT: BRUCE R. ZETTER AND LERE BAO
; TITLE OF INVENTION: HUMAN THYMOSIN 15 GENE,
; CORRESPONDENCE ADDRESS: PROTEIN AND USES THEREOF
; NUMBER OF SEQUENCES: 13
; ADDRESS: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
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OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA: US/09/874,736
APPLICATION NUMBER: US/09/874,736
FILING DATE: 19-NO. US20020183496A1-2001
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/801,796
FILING DATE: 14-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 46507
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-874-736-8

Query Match 5.8%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATCAGTAGTGGCTGCACCCGCG 24
|||||
DB 1 TATCAGTAGTGGCTGCACCCGCG 24

RESULT 13
US-09-874-736-9/c
Sequence 9, Application US/09874736
Publication No. US20020183496A1
GENERAL INFORMATION:
APPLICANT: BRUCE R. ZETTER AND LERE BAO
TITLE OF INVENTION: HUMAN THYMOSIN 15 GENE,
PROTEIN AND USES THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/874,736
FILING DATE: 19-NO. US20020183496A1-2001
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/801,796
FILING DATE: 14-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 46507
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-874-736-9

Query Match 5.8%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 ACCCTGACTGAAAGTCAGCATTT 379
|||||
DB 24 ACCCTGACTGAAAGTCAGCATTT 1

RESULT 14
US-10-726-422-8
Sequence 8, Application US/10726422
Publication No. US20040101910A1
GENERAL INFORMATION:
APPLICANT: BRUCE R. ZETTER AND LERE BAO
TITLE OF INVENTION: HUMAN THYMOSIN 15 GENE,
PROTEIN AND USES THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/726,422
FILING DATE: 03-DEC-2003
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/801,796
FILING DATE: 14-FEB-1997
APPLICATION NUMBER: 08/664,856
FILING DATE: 17 JUN 1996
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 46507
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO

FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-726-422-8

Search completed: March 12, 2006, 06:57:44
Job time : 795 secs

Query Match 5.8%; Score 24; DB 7; Length 24;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATCAGCTAGTGGCTGCACCCGCG 24
Db 1 TATCAGCTAGTGGCTGCACCCGCG 24

RESULT 15

US-10-726-422-9/c
; Sequence 9, Application US/10726422
; Publication No. US20040101910A1
; GENERAL INFORMATION:
; APPLICANT: BRUCE R. ZETTER AND LERE BAO
; TITLE OF INVENTION: HUMAN THYMOSIN 15 GENE,
; PROTEIN AND USES THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA: US/10/726,422
; FILING DATE: 03-Dec-2003
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,796
; FILING DATE: 14-FEB-1997
; APPLICATION NUMBER: 08/664,856
; FILING DATE: 17 JUN 1996

ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 46507
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:

SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-726-422-9
Query Match 5.8%; Score 24; DB 7; Length 24;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 356 ACCCTGACTGAAGGTCAGCATTT 379
Db 24 ACCCTGACTGAAGGTCAGCATTT 1

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OM nucleic - nucleic search, using sw model

Run on: March 12, 2006, 05:58:46 ; Search time 328 Seconds
(without alignments)
2898.190 Million cell updates/sec

Title: US-10-726-422-1
Perfect score: 412
Sequence: 1 TATCAGCTAGTGGTGCACC.....AAATGTGTTTCCACTGCTC 412

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7673375 seqs, 115364844 residues

Total number of hits satisfying chosen parameters: 12400308

Minimum DB seq length: 10
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA_New.*
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2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
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11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.8	5.3	25	12	US-11-121-849-515721 Sequence 515721, Sequence 90, Appl
2	20.2	4.9	25	12	US-11-113-424-90 Sequence 90, Appl
3	19.4	4.7	25	12	US-11-121-849-284665 Sequence 284665,
C 4	18.6	4.5	25	12	US-11-121-849-340130 Sequence 340130,
C 5	18.2	4.4	25	7	US-10-932-182A-89391 Sequence 89391, A
C 6	18.2	4.4	25	7	US-10-932-182A-89391 Sequence 89391, A
C 7	18.2	4.4	25	12	US-11-121-849-262586 Sequence 262586,
8	18	4.4	19	10	US-11-101-244-773890 Sequence 773890,
9	18	4.4	19	11	US-11-083-784-773890 Sequence 773890,
10	18	4.4	26	8	US-10-310-914A-1060248 Sequence 1060248,
C 11	17.8	4.3	25	12	US-11-121-849-89187 Sequence 89187, A
C 12	17.8	4.3	25	12	US-11-121-849-210505 Sequence 210505,
C 13	17.8	4.3	25	12	US-11-121-849-210506 Sequence 210506,
C 14	17.8	4.3	25	12	US-11-121-849-210507 Sequence 210507,
15	17.6	4.3	25	7	US-10-932-182A-145807 Sequence 145807,
16	17.6	4.3	25	7	US-10-932-182A-145807 Sequence 145807,
C 17	17.6	4.3	25	12	US-11-121-849-46145 Sequence 46145, A
C 18	17.6	4.3	25	12	US-11-121-849-50711 Sequence 50711, A
C 19	17.6	4.3	25	12	US-11-121-849-239869 Sequence 239869,
C 20	17.6	4.3	25	12	US-11-121-849-301096 Sequence 301096,

C	21	17.6	4.3	25	12	US-11-121-849-407098 Sequence 407098,
	22	17.6	4.3	35	8	US-10-489-866-7 Sequence 7, Appl
	23	17.4	4.2	19	10	US-11-101-244-324658 Sequence 324658,
	24	17.4	4.2	19	10	US-11-101-244-324704 Sequence 324704,
	25	17.4	4.2	19	10	US-11-101-244-324789 Sequence 324789,
	26	17.4	4.2	19	11	US-11-083-784-324658 Sequence 324658,
	27	17.4	4.2	19	11	US-11-083-784-324704 Sequence 324704,
	28	17.4	4.2	19	11	US-11-083-784-324789 Sequence 324789,
	29	17.4	4.2	27	8	US-10-310-914A-957870 Sequence 957870,
	30	17.4	4.2	36	12	US-11-100-553B-28 Sequence 28, Appl
	31	17.2	4.2	22	8	US-10-310-914A-151755 Sequence 151755,
	32	17.2	4.2	25	7	US-10-932-182A-130334 Sequence 130334,
	33	17.2	4.2	25	7	US-10-932-182A-130334 Sequence 130334,
	34	17.2	4.2	25	8	US-10-310-914A-151780 Sequence 151780,
	35	17.2	4.2	25	8	US-10-310-914A-1024160 Sequence 1024160,
	36	17.2	4.2	25	8	US-10-310-914A-1024161 Sequence 1024161,
	37	17.2	4.2	25	12	US-11-121-849-333427 Sequence 333427,
	38	17.2	4.2	25	12	US-11-121-849-507249 Sequence 507249,
	39	17.2	4.2	25	12	US-11-136-527-128712 Sequence 128712,
	40	17.2	4.2	25	12	US-11-136-527-128718 Sequence 128718,
C	41	17.2	4.2	25	12	US-11-136-527-343395 Sequence 343395,
C	42	17.2	4.2	30	8	US-10-750-185-14851 Sequence 14851, A
C	43	17.2	4.2	30	8	US-10-750-623-14851 Sequence 14851, A
	44	17	4.1	19	10	US-11-101-244-773898 Sequence 773898,
	45	17	4.1	19	11	US-11-083-784-773898 Sequence 773898,

ALIGNMENTS

RESULT 1
US-11-121-849-515721
; Sequence 515721, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded St
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 515721
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-515721

Query Match	5.3%	Score 21.8;	DB 12;	Length 25;
Best Local Similarity	92.0%	Pred. No. 3.1e+04;		
Matches	23;	Conservative	0;	Mismatches 2;
			Indels	0;
			Gaps	0;
Qy	177	ATACTCTTCCTCGAAGAACTAT 201		
Db	1	ATACTCTTCCTCGAAGAACTAT 25		
RESULT 2				
US-11-113-424-90				
; Sequence 90, Application US/11113424				
; Publication No. US20050260713A1				
; GENERAL INFORMATION:				
; APPLICANT: Gangolli et al.				
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same				
; FILE REFERENCE: 21402-225				
; CURRENT APPLICATION NUMBER: US/11/113,424				
; CURRENT FILING DATE: 2005-04-21				
; PRIOR APPLICATION NUMBER: 60/256,704				
; PRIOR FILING DATE: 2000-12-19				
; PRIOR APPLICATION NUMBER: 60/311,590				

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; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 90
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR primer
US-11-113-424-90
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Query Match          4.9%; Score 20.2; DB 12; Length 25;
Best Local Similarity 88.0%; Pred. No. 7.4e+04;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 98 ATGAGTGATAAACCAAGACTTATCAG 122
      |||||
Db 1 ATGAGTGATAAACCAAGACTTGTGAC 25
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RESULT 3
US-11-121-849-284665
; Sequence 284665, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 284665
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-284665
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Query Match          4.7%; Score 19.4; DB 12; Length 25;
Best Local Similarity 95.2%; Pred. No. 1.2e+05;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 292 ACATGTTTCTGTAACCTTATC 312
      |||||
Db 4 ACATGTTTCTGTAACCTTATC 24
```

```
RESULT 4
US-11-121-849-340130/c
; Sequence 340130, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
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; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 340130
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-340130
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Query Match          4.5%; Score 18.6; DB 12; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.8e+05;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 193 GGAACCTATCCAGCAGGAGAAAGAA 217
      |||||
Db 25 GGAATGATTCAGCGGAGAAAGAA 1
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```
RESULT 5
US-10-932-182A-89391/c
; Sequence 89391, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 89391
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-89391
```

```
Query Match          4.4%; Score 18.2; DB 7; Length 25;
Best Local Similarity 87.0%; Pred. No. 2.2e+05;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 225 AAAGATCATAAATGAGATTCTC 247
      |||||
Db 25 AAAGATAATGAAAAGAGATTCTC 3
```

```
RESULT 6
US-10-932-182A-89391/c
; Sequence 89391, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 89391
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-89391
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Query Match 4.4%; Score 18.2; DB 7; Length 25;
Best Local Similarity 87.0%; Pred. No. 2.2e+05;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 225 AAAGATCATATAATGAGATTCTC 247
|||||
DB 25 AAAGATCATATAATGAGATTCTC 3

RESULT 7
US-11-121-849-262586/c
; Sequence 262586, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 262586
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-262586

Query Match 4.4%; Score 18.2; DB 12; Length 25;
Best Local Similarity 87.0%; Pred. No. 2.2e+05;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 214 AGAATATAATCAAGATCATATAA 236
|||||
DB 24 AGAATATACTCAAGATCAAAAA 2

RESULT 8
US-11-101-244-773890
; Sequence 773890, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 773890
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-773890

Query Match 4.4%; Score 18; DB 10; Length 19;
Best Local Similarity 77.8%; Pred. No. 2.3e+05;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 91 AGTCAAGATGAGTGATTA 108
|||||

Db 2 AGUCAAGAUGAGUGAUAA 19
RESULT 9
US-11-083-784-773890
; Sequence 773890, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 773890
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-773890

Query Match 4.4%; Score 18; DB 11; Length 19;
Best Local Similarity 77.8%; Pred. No. 2.3e+05;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 91 AGTCAAGATGAGTGATTA 108
|||||
DB 2 AGUCAAGAUGAGUGAUAA 19

RESULT 10
US-10-310-914A-1060248
; Sequence 1060248, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patent version 3.3
; SEQ ID NO 1060248
; LENGTH: 26
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1060248

Query Match 4.4%; Score 18; DB 8; Length 26;
Best Local Similarity 73.1%; Pred. No. 2.5e+05;
Matches 19; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 199 TATCCAGCAGGAGAGAAATATATC 224
:|:|||||
DB 1 UAUACAGCAGGAGAGAAATATATC 26

RESULT 11
US-11-121-849-89187/c
; Sequence 89187, Application US/11121849

```

; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 89187
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-89187

Query Match
Best Local Similarity 4.3%; Score 17.8; DB 12; Length 25;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 217 ATATAATCAAGATCATATAA 237
Db 23 AGATAATCAAGAGCATATAA 3

RESULT 12
US-11-121-849-210505/c
; Sequence 210505, Application US/11/121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 210505
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-210505

Query Match
Best Local Similarity 4.3%; Score 17.8; DB 12; Length 25;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 144 CAAAGTTGAAGAGACTTAATA 164
Db 24 CAAAGGTGAAGAGACTTAATA 4

RESULT 13
US-11-121-849-210506/c
; Sequence 210506, Application US/11/121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 210506
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-210506

Query Match
Best Local Similarity 4.3%; Score 17.8; DB 12; Length 25;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 144 CAAAGTTGAAGAGACTTAATA 164
Db 24 CAAAGGTGAAGAGACTTAATA 4

RESULT 14
US-11-121-849-210507/c
; Sequence 210507, Application US/11/121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 210507
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-210507

Query Match
Best Local Similarity 4.3%; Score 17.8; DB 12; Length 25;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 144 CAAAGTTGAAGAGACTTAATA 164
Db 21 CAAAGGTGAAGAGACTTAATA 1

RESULT 15
US-10-932-182A-145807
; Sequence 145807, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 145807
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-145807

Query Match
Best Local Similarity 4.3%; Score 17.6; DB 7; Length 25;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 60 TTGCTGGCCTAGTAGAAGCTTTGG 83
Db 2 TTGTTGGCATACCAAGACTTTGG 25

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; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 89187
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-89187

Query Match      4.3%; Score 17.8; DB 12; Length 25;
Best Local Similarity 90.5%; Pred. No. 2.8e+05;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      217 ATATAATCAAGATCATATAAA 237
Db      23 AGATAATCAAGAGCATATAAA 3

RESULT 12
US-11-121-849-210505/c
; Sequence 210505, Application US/11/121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 210505
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-210505

Query Match      4.3%; Score 17.8; DB 12; Length 25;
Best Local Similarity 90.5%; Pred. No. 2.8e+05;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      144 CAAAGTTGAAGAGACTTAATA 164
Db      24 CAAAGGTGAAGAGACTTAATA 4

RESULT 13
US-11-121-849-210506/c
; Sequence 210506, Application US/11/121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 210506
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-210506

Query Match      4.3%; Score 17.8; DB 12; Length 25;
Best Local Similarity 90.5%; Pred. No. 2.8e+05;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      144 CAAAGTTGAAGAGACTTAATA 164
Db      24 CAAAGGTGAAGAGACTTAATA 4

RESULT 14
US-11-121-849-210507/c
; Sequence 210507, Application US/11/121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 210507
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-210507

Query Match      4.3%; Score 17.8; DB 12; Length 25;
Best Local Similarity 90.5%; Pred. No. 2.8e+05;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      144 CAAAGTTGAAGAGACTTAATA 164
Db      21 CAAAGGTGAAGAGACTTAATA 1

RESULT 15
US-10-932-182A-145807
; Sequence 145807, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 145807
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-145807

Query Match      4.3%; Score 17.6; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 3.1e+05;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      60 TTGCTGGCCTAGTAGAAGCTTTGG 83
Db      2 TTGTTGGCATACCAAGCTTTGG 25

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Search completed: March 12, 2006, 06:49:29
Job time : 328 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 12, 2006, 00:39:01 ; Search time 155 Seconds
(without alignments)
4724.874 Million cell updates/sec

Title: US-10-726-422-1
Perfect score: 412
Sequence: 1 TATCAGTAGTGGTCACCC.....AAATGTGTTTCCACTGCTC 412

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1188356

Minimum DB seq length: 10
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/prodata/1/ina/1 COMB.seq.*
2: /cgn2_6/prodata/1/ina/5 COMB.seq.*
3: /cgn2_6/prodata/1/ina/6A COMB.seq.*
4: /cgn2_6/prodata/1/ina/6B COMB.seq.*
5: /cgn2_6/prodata/1/ina/H COMB.seq.*
6: /cgn2_6/prodata/1/ina/PCUS COMB.seq.*
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8: /cgn2_6/prodata/1/ina/RE COMB.seq.*
9: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	5.8	24	2	Sequence 8, Appl
2	24	5.8	24	2	Sequence 9, Appl
3	24	5.8	24	2	Sequence 8, Appl
4	24	5.8	24	2	Sequence 9, Appl
5	24	5.8	24	2	Sequence 8, Appl
6	24	5.8	24	2	Sequence 9, Appl
7	24	5.8	24	2	Sequence 3, Appl
8	24	5.8	24	2	Sequence 4, Appl
9	24	5.8	24	3	Sequence 8, Appl
10	24	5.8	24	3	Sequence 9, Appl
11	24	5.8	24	3	Sequence 3, Appl
12	24	5.8	24	3	Sequence 8, Appl
13	24	5.8	24	3	Sequence 9, Appl
14	24	5.8	24	3	Sequence 8, Appl
15	20.4	5.0	36	3	Sequence 374, App
16	20.4	5.0	36	3	Sequence 374, App
17	20.4	5.0	36	3	Sequence 374, App
18	20.4	5.0	36	6	Sequence 374, App
19	19.2	4.7	33	3	Sequence 75, Appl
20	19.2	4.7	33	3	Sequence 75, Appl
21	19.2	4.7	33	3	Sequence 75, Appl
22	19.2	4.7	33	3	Sequence 75, Appl
23	19.2	4.7	33	3	Sequence 75, Appl
24	19.2	4.7	33	3	Sequence 75, Appl

c 25	19	4.6	36	2	US-08-411-796-384	Sequence 384, App
c 26	19	4.6	36	3	US-08-471-039-384	Sequence 384, App
c 27	19	4.6	36	3	US-08-559-390-384	Sequence 384, App
c 28	19	4.6	36	6	PCT-US93-11198-384	Sequence 384, App
c 29	18.8	4.6	36	2	US-08-411-796-376	Sequence 376, App
c 30	18.8	4.6	36	2	US-08-411-796-378	Sequence 378, App
c 31	18.8	4.6	36	2	US-08-411-796-380	Sequence 380, App
c 32	18.8	4.6	36	2	US-08-411-796-386	Sequence 386, App
c 33	18.8	4.6	36	3	US-08-471-039-376	Sequence 376, App
c 34	18.8	4.6	36	3	US-08-471-039-378	Sequence 378, App
c 35	18.8	4.6	36	3	US-08-471-039-380	Sequence 380, App
c 36	18.8	4.6	36	3	US-08-471-039-386	Sequence 386, App
c 37	18.8	4.6	36	3	US-08-559-390-376	Sequence 376, App
c 38	18.8	4.6	36	3	US-08-559-390-378	Sequence 378, App
c 39	18.8	4.6	36	3	US-08-559-390-380	Sequence 380, App
c 40	18.8	4.6	36	3	US-08-559-390-386	Sequence 386, App
c 41	18.8	4.6	36	6	PCT-US93-11198-376	Sequence 376, App
c 42	18.8	4.6	36	6	PCT-US93-11198-378	Sequence 378, App
c 43	18.8	4.6	36	6	PCT-US93-11198-380	Sequence 380, App
c 44	18.8	4.6	36	6	PCT-US93-11198-386	Sequence 386, App
c 45	18.6	4.5	31	2	US-08-829-961-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-664-856A-8
; Sequence 8, Application US/08664856A
; Patent No. 563071
; GENERAL INFORMATION:
; APPLICANT: BRUCE R. ZETTER AND LERE BAO
; TITLE OF INVENTION: HUMAN THYMOSIN 15 GENE,
; TITLE OF INVENTION: PROTEIN AND USES THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/664,856A
; FILING DATE: 17 JUN 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 46507
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:

US-08-664-856A-8

Query Match 5.8%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATCAGCTAGTGGCTGCACCCGCG 24
|||||
Db 1 TATCAGCTAGTGGCTGCACCCGCG 24

RESULT 2

US-08-664-856A-9/c
; Sequence 9, Application US/08664856A
; Patent No. 5663071

; GENERAL INFORMATION:

; APPLICANT: BRUCE R. ZETTER AND LERE BAO
; TITLE OF INVENTION: HUMAN THYMOSIN 15 GENE,
; TITLE OF INVENTION: PROTEIN AND USES THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/664,856A
; FILING DATE: 17 JUN 1996
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 46507
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 24 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE:

; ORIGINAL SOURCE:

US-08-664-856A-9

Query Match 5.8%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 356 ACCCTGACTGAAAGTCAGCATTT 379
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Db 24 ACCCTGACTGAAAGTCAGCATTT 1

RESULT 3

US-08-801-796-8
; Sequence 8, Application US/08801796
; Patent No. 5721337

; GENERAL INFORMATION:

; APPLICANT: BRUCE R. ZETTER AND LERE BAO
; TITLE OF INVENTION: HUMAN THYMOSIN 15 GENE,
; TITLE OF INVENTION: PROTEIN AND USES THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/801,796
; FILING DATE: 14-FEB-1997
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/664,856
; FILING DATE: 17 JUN 1996
; ATTORNEY/AGENT INFORMATION:

; NAME: DAVID, RESNICK S

; REGISTRATION NUMBER: 34,235

; REFERENCE/DOCKET NUMBER: 46507

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-523-3400

; TELEFAX: 617-523-6440

; TELEX: 200291 STRE

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 24 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE:

; ORIGINAL SOURCE:

US-08-801-796-8

Query Match 5.8%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATCAGCTAGTGGCTGCACCCGCG 24
|||||
Db 1 TATCAGCTAGTGGCTGCACCCGCG 24

RESULT 4

US-08-801-796-9/c

; Sequence 9, Application US/08801796
; Patent No. 5721337

; GENERAL INFORMATION:

; APPLICANT: BRUCE R. ZETTER AND LERE BAO
; TITLE OF INVENTION: HUMAN THYMOSIN 15 GENE,
; TITLE OF INVENTION: PROTEIN AND USES THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,796
FILING DATE: 14-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/664,856
FILING DATE: 17 JUN 1996
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 46507
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-801-796-9

Query Match 5.8%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 ACCCTGACTGAAAGTTCAGCATTT 379
DB 24 ACCCTGACTGAAAGTTCAGCATTT 1

RESULT 5
US-08-931-877-8
Sequence 8, Application US/08931877
Patent No. 5831033
GENERAL INFORMATION:
APPLICANT: BRUCE R. ZETTER AND LERE BAO
TITLE OF INVENTION: HUMAN THYMOSIN 15 GENE,
TITLE OF INVENTION: PROTEIN AND USES THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,877
FILING DATE: 17-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/801,796
FILING DATE: 14-FEB-1997
APPLICATION NUMBER: 08/664,856
FILING DATE: 17 JUN 1996
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 46507

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-931-877-8

Query Match 5.8%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATCAGCTAGTGGCTGCACCCGCG 24
DB 1 TATCAGCTAGTGGCTGCACCCGCG 24

RESULT 6
US-08-931-877-9/c
Sequence 9, Application US/08931877
Patent No. 5831033
GENERAL INFORMATION:
APPLICANT: BRUCE R. ZETTER AND LERE BAO
TITLE OF INVENTION: HUMAN THYMOSIN 15 GENE,
TITLE OF INVENTION: PROTEIN AND USES THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,877
FILING DATE: 17-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/801,796
FILING DATE: 14-FEB-1997
APPLICATION NUMBER: 08/664,856
FILING DATE: 17 JUN 1996
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 46507
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO

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; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-931-877-9

Query Match      5.8%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 356 ACCCTGACTGAAGGTCAGCATTT 379
Db 24 ACCCTGACTGAAGGTCAGCATTT 1

RESULT 7
US-08-664-857A-3
; Sequence 3, Application US/08664857A
; Patent No. 5858681
; GENERAL INFORMATION:
; APPLICANT: BRUCE R. ZETTER AND LERE BAO
; TITLE OF INVENTION: A METHOD FOR DIAGNOSIS AND PROGNOSIS OF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/664,857A
; FILING DATE: 17 JUN 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 46403
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-664-857A-4

Query Match      5.8%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 356 ACCCTGACTGAAGGTCAGCATTT 379
Db 24 ACCCTGACTGAAGGTCAGCATTT 1

RESULT 9
US-08-069-484-8
; Sequence 8, Application US/09069484
; Patent No. 6017717
; GENERAL INFORMATION:
; APPLICANT: BRUCE R. ZETTER AND LERE BAO
; TITLE OF INVENTION: HUMAN THYMOSIN 15 GENE,
; TITLE OF INVENTION: PROTEIN AND USES THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
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;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSEQ Version 1.5
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/069,484
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/801,796
;; FILING DATE: 14-FEB-1997
;; APPLICATION NUMBER: 08/664,856
;; FILING DATE: 17 JUN 1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: DAVID, RESNICK S
;; REGISTRATION NUMBER: 34,235
;; REFERENCE/DOCKET NUMBER: 46507
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-523-3400
;; TELEFAX: 617-523-6440
;; TELEX: 200291 STRE
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 24 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; US-09-069-484-8

Query Match 5.8%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATCAGCTAGTGGCTGCACCCGCG 24
|||||
DB 1 TATCAGCTAGTGGCTGCACCCGCG 24

RESULT 10
US-09-069-484-9/c
; Sequence 9, Application US/09069484
; Patent No. 6017717
; GENERAL INFORMATION:
; APPLICANT: BRUCE R. ZETTER AND LERE BAO
; TITLE OF INVENTION: HUMAN THYMOSIN 15 GENE,
; TITLE OF INVENTION: PROTEIN AND USES THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,484
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/801,796
; FILING DATE: 14-FEB-1997
; APPLICATION NUMBER: 08/664,856
; FILING DATE: 17 JUN 1996

;; ATTORNEY/AGENT INFORMATION:
;; NAME: DAVID, RESNICK S
;; REGISTRATION NUMBER: 34,235
;; REFERENCE/DOCKET NUMBER: 46507
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-523-3400
;; TELEFAX: 617-523-6440
;; TELEX: 200291 STRE
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 24 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; US-09-069-484-9

Query Match 5.8%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 ACCCTGACTGAAAGGTCAGCATTT 379
|||||
DB 24 ACCCTGACTGAAAGGTCAGCATTT 1

RESULT 11
US-09-135-599-3
; Sequence 3, Application US/09135599
; Patent No. 6150117
; GENERAL INFORMATION:
; APPLICANT: BRUCE R. ZETTER AND LERE BAO
; TITLE OF INVENTION: A METHOD FOR DIAGNOSIS AND PROGNOSIS OF
; TITLE OF INVENTION: CANCER
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,599
; FILING DATE: 18 AUG 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/664,857
; FILING DATE: 17 JUN 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 46403
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE:
 ; ORIGINAL SOURCE:
 US-09-135-599-3

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Query Match      5.8%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 TATCAGCTAGTGGCTGCACCCGCG 24
|||
Db 1 TATCAGCTAGTGGCTGCACCCGCG 24

RESULT 12
 US-09-135-599-4/c
 ; Sequence 4, Application US/09135599
 ; Patent No. 6150117
 ; GENERAL INFORMATION:
 ; APPLICANT: BRUCE R. ZETTER AND LERE BAO
 ; TITLE OF INVENTION: A METHOD FOR DIAGNOSIS AND PROGNOSIS OF
 ; TITLE OF INVENTION: CANCER
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
 ; STREET: 130 WATER STREET
 ; CITY: BOSTON
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02019

Query Match	5.8%	Score 24;	DB 3;	Length 24;
Best Local Similarity	100.0%;	Pred. No. 7.6e+02;		
Matches 24;	Conservative	0;	Mismatches 0;	Indels 0;
				Gaps 0;

QY 356 ACCCTGACTGAAAGGTCAGCATT 379
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Db 24 ACCCTGACTGAAAGGTCAGCATT 1

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Query Match	5.8%	Score 24;	DB 3;	Length 24;
Best Local Similarity	100.0%;	Pred. No. 7.6e+02;		
Matches 24;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 TATCAGCTAGTGGCTGCACCCGCG 24
|||
Db 1 TATCAGCTAGTGGCTGCACCCGCG 24

RESULT 14
US-09-369-744-9/c
; Sequence 9, Application US/09369744
; Patent No. 6300479
; GENERAL INFORMATION:
; APPLICANT: BRUCE R. ZETTER AND LERE BAO
; TITLE OF INVENTION: HUMAN THYMOSIN 15 GENE,
; TITLE OF INVENTION: PROTEIN AND USES THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA

;; ZIP: 02019
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq Version 1.5
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/369,744
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; PRIOR APPLICATION NUMBER: 08/801,796
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: DAVID, RESNICK S
;; REGISTRATION NUMBER: 34,235
;; REFERENCE/DOCKET NUMBER: 46507
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-523-3400
;; TELEFAX: 617-523-6440
;; TELEX: 200291 STR
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 24 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; US-09-369-744-9

Query Match 5.8%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 ACCCTGACTGAAAGGTCAGCATTT 379
DB 24 ACCCTGACTGAAAGGTCAGCATTT 1

RESULT 15
US-08-411-796-374/c
; Sequence 374, Application US/08411796
; Patent No. 5677149
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Caparon, Mairé H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olin, Peter O.
; APPLICANT: Polak, Kuman
; APPLICANT: Polazzi, Joseph O.
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Interleukin-3 (IL-3) Mutant Polypeptides
; NUMBER OF SEQUENCES: 549
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESSEE: Corporate Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/411,796
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; PRIOR APPLICATION NUMBER: US 07/981044
;; FILING DATE: 24-NOV-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US93/11198
;; FILING DATE: 22-NOV-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bennett, Dennis A.
;; REGISTRATION NUMBER: 34,547
;; REFERENCE/DOCKET NUMBER: C2713/1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (708)470-6501
;; TELEFAX: (708)470-6881
;; INFORMATION FOR SEQ ID NO: 374:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 36 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (synthetic)
;; US-08-411-796-374

Query Match 5.0%; Score 20.4; DB 2; Length 36;
Best Local Similarity 80.0%; Pred. No. 1.1e+04;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 181 TCTTCCTTCGAAGAACTATCCAGCAGGA 210
DB 31 TGTTCCTTCGAAGGTTATTTCCATCAGGA 2

Search completed: March 12, 2006, 00:52:48
Job time : 155 secs

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